

SEQUENCE LISTING

<110> Hart, Charles E.
Topouzis, Stavros
Gilbertson, Debra G.

<120> METHOD OF TREATING FIBROPROLIFERATIVE
DISORDERS

<130> 00-79

<150> US 60/235,295
<151> 2000-09-26

<150> US 09/564,595
<151> 2000-05-03

<150> US 60/180,169
<151> 2000-02-04

<150> US 60/164,463
<151> 1999-11-10

<150> US 60/132,250
<151> 1999-05-03

<160> 13

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 1882
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (226)...(1338)

<400> 1

ccgtcaccat ttatcagctc agcaccacaa ggaagtgcgg caccacacg cgctcgaaaa
gttcagcatg caggaagttt gggagagct cggcgattag cacagcggacc cgggccagcg

60

120

cagggcgagc gcagggcgcg agagcgcagg gcggcgccgc gtcggtcccg ggagcagaac ccggctttt cttggagcga cgctgtctct agtcgtgtat cccaa atg cac cgg ctc Met His Arg Leu	180 237
1	
atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp	285
5 10 15	20
act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala	333
25 30 35	
aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg	381
40 45 50	
gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg	429
55 60 65	
ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Thr Trp Arg Leu His	477
70 75 80	
tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly	525
85 90 95 100	
tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val	573
105 110 115	
gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly	621
120 125 130	
cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys	669
135 140 145	

atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag	717		
Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys			
150	155	160	
att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag	765		
Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ser Glu			
165	170	175	180
acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac	813		
Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn			
185	190	195	
tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa	861		
Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys			
200	205	210	
aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat	909		
Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn			
215	220	225	
cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct	957		
Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro			
230	235	240	
cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg	1005		
Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu			
245	250	255	260
gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat	1053		
Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn			
265	270	275	
tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc	1101		
Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe			
280	285	290	
ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt	1149		
Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys			
295	300	305	
gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg	1197		
Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val			
310	315	320	

aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg	1245
Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg	
325 330 335 340	
agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac	1293
Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His	
345 350 355	
cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa	1338
His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *	
360 365 370	
gagaatgtgc acatccttac attaaggcctg aaagaacctt tagtttaagg agggtgagat	1398
aagagaccct tttccttacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca	1458
agtgggtgct gagtctcagc cttgctttgt taatgccatg gcaagtagaa aggtatata	1518
tcaacttcta tacctaagaa tataggattt catttaataa tagtggatgg gtttatata	1578
gcacaaacac acacagaaat atattcatgt ctatgtgtat atagatcaa tttttttt	1638
ttttggtata tataacccagg tacaccagag gttacatatg tttgagttt actcttaaaa	1698
tcctttgcca aaataaggga tggtaaata tatgaaacat gtcttttagaa aatttaggag	1758
ataaaatttat ttttaaattt tgaaacacga aacaattttg aatcttgctc tcttaaagaa	1818
agcatcttgt atattaaaaa tcaaaagatg aggctttctt acatatacat ctttagttgat	1878
tatt	1882

<210> 2

<211> 370

<212> PRT

<213> Homo sapiens

<400> 2

Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys	
1 5 10 15	
Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala	
20 25 30	
Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp	
35 40 45	
Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val	
50 55 60	
Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Thr	
65 70 75 80	
Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp	
85 90 95	

Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
 100 105 110
 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
 115 120 125
 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
 130 135 140
 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
 145 150 155 160
 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
 165 170 175
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
 180 185 190
 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
 195 200 205
 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 210 215 220
 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
 225 230 235 240
 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 245 250 255
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
 260 265 270
 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
 275 280 285
 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 290 295 300
 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
 305 310 315 320
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
 325 330 335
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
 340 345 350
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
 355 360 365
 Pro Arg
 370

<210> 3
 <211> 1472
 <212> DNA
 <213> Mus musculus

<220>

<221> CDS

<222> (93)...(1205)

<400> 3

agggactgtg cagtagaaat ccggccgactc aaccctttgg gctttatTTTA tttacttttg 60
 gagcaacgcg atcccttaggt cgctgagccc aa atg caa cgg ctc gtt tta gtc 113
 Met Gln Arg Leu Val Leu Val
 1 5

tcc att ctc ctg tgc gcg aac ttt agc tgc tat ccg gac act ttt gcg 161
 Ser Ile Leu Leu Cys Ala Asn Phe Ser Cys Tyr Pro Asp Thr Phe Ala
 10 15 20

act ccg cag aga gca tcc atc aaa gct ttg cgc aat gcc aac ctc agg 209
 Thr Pro Gln Arg Ala Ser Ile Lys Ala Leu Arg Asn Ala Asn Leu Arg
 25 30 35

aga gat gag agc aat cac ctc aca gac ttg tac cag aga gag gag aac 257
 Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Gln Arg Glu Glu Asn
 40 45 50 55

att cag gtg aca agc aat ggc cat gtg cag agt cct cgc ttc ccg aac 305
 Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro Asn
 60 65 70

agc tac cca agg aac ctg ctt ctg aca tgg tgg ctc cgt tcc cag gag 353
 Ser Tyr Pro Arg Asn Leu Leu Thr Trp Trp Leu Arg Ser Gln Glu
 75 80 85

aaa aca cgg ata caa ctg tcc ttt gac cat caa ttc gga cta gag gaa 401
 Lys Thr Arg Ile Gln Leu Ser Phe Asp His Gln Phe Gly Leu Glu Glu
 90 95 100

gca gaa aat gac att tgt agg tat gac ttt gtg gaa gtt gaa gaa gtc 449
 Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Val
 105 110 115

tca gag agc agc act gtt gtc aga gga aga tgg tgt ggc cac aag gag 497
 Ser Glu Ser Ser Thr Val Val Arg Gly Arg Trp Cys Gly His Lys Glu
 120 125 130 135

atc cct cca agg ata acg tca aga aca aac cag att aaa atc aca ttt			545
Ile Pro Pro Arg Ile Thr Ser Arg Thr Asn Gln Ile Lys Ile Thr Phe			
140	145	150	
aag tct gat gac tac ttt gtg gca aaa cct gga ttc aag att tat tat			593
Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys Ile Tyr Tyr			
155	160	165	
tca ttt gtg gaa gat ttc caa ccg gaa gca gcc tca gag acc aac tgg			641
Ser Phe Val Glu Asp Phe Gln Pro Glu Ala Ala Ser Glu Thr Asn Trp			
170	175	180	
gaa tca gtc aca agc tct ttc tct ggg gtg tcc tat cac tct cca tca			689
Glu Ser Val Thr Ser Ser Phe Ser Gly Val Ser Tyr His Ser Pro Ser			
185	190	195	
ata acg gac ccc act ctc act gct gat gcc ctg gac aaa act gtc gca			737
Ile Thr Asp Pro Thr Leu Thr Ala Asp Ala Leu Asp Lys Thr Val Ala			
200	205	210	215
gaa ttc gat acc gtg gaa gat cta ctt aag cac ttc aat cca gtg tct			785
Glu Phe Asp Thr Val Glu Asp Leu Leu Lys His Phe Asn Pro Val Ser			
220	225	230	
tgg caa gat gat ctg gag aat ttg tat ctg gac acc cct cat tat aga			833
Trp Gln Asp Asp Leu Glu Asn Leu Tyr Leu Asp Thr Pro His Tyr Arg			
235	240	245	
ggc agg tca tac cat gat cgg aag tcc aaa gtg gac ctg gac agg ctc			881
Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu			
250	255	260	
aat gat gat gtc aag cgt tac agt tgc act ccc agg aat cac tct gtg			929
Asn Asp Asp Val Lys Arg Tyr Ser Cys Thr Pro Arg Asn His Ser Val			
265	270	275	
aac ctc agg gag gag ctg aag ctg acc aat gca gtc ttc ttc cca cga			977
Asn Leu Arg Glu Glu Leu Lys Leu Thr Asn Ala Val Phe Phe Pro Arg			
280	285	290	295
tgc ctc ctc gtg cag cgc tgt ggt ggc aac tgt ggt tgc gga act gtc			1025
Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val			
300	305	310	

aac tgg aag tcc tgc aca tgc agc tca ggg aag aca gtg aag aag tat 1073
Asn Trp Lys Ser Cys Thr Cys Ser Ser Gly Lys Thr Val Lys Lys Tyr
315 320 325

cat gag gta ttg aag ttt gag cct gga cat ttc aag aga agg ggc aaa 1121
His Glu Val Leu Lys Phe Glu Pro Gly His Phe Lys Arg Arg Gly Lys
330 335 340

gct aag aat atg gct ctt gtt gat atc cag ctg gat cat cat gag cga 1169
Ala Lys Asn Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg
345 350 355

tgt gac tgt atc tgc agc tca aga cca cct cga taa aacactatgc 1215
 Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

acatctgtac tttgattatg aaaggacctt tagttacaa aaaccctaag aagcttctaa 1275
tctcagtgc aatgtatgtatgaaatgt tgctttgtta gtgcctatggc aagaagaagc 1335
aaatatcatt aatttctata tacataaaca taggaattca ctatcaata gtatgtgaag 1395
atatgtatata tatacttatacatgacttag ctctatgtat gtaaatagat taaatacttt 1455
attcagtata tttactg 1472

<210> 4

<211> 370

<212> PRT

<213> *Mus musculus*

,<400> 4

Met	Gln	Arg	Leu	Val	Leu	Val	Ser	Ile	Leu	Leu	Cys	Ala	Asn	Phe	Ser
1				5					10					15	
Cys	Tyr	Pro	Asp	Thr	Phe	Ala	Thr	Pro	Gln	Arg	Ala	Ser	Ile	Lys	Ala
					20				25					30	
Leu	Arg	Asn	Ala	Asn	Leu	Arg	Arg	Asp	Glu	Ser	Asn	His	Leu	Thr	Asp
					35			40					45		
Leu	Tyr	Gln	Arg	Glu	Glu	Asn	Ile	Gln	Val	Thr	Ser	Asn	Gly	His	Val
					50			55					60		
Gln	Ser	Pro	Arg	Phe	Pro	Asn	Ser	Tyr	Pro	Arg	Asn	Leu	Leu	Leu	Thr
					65			70					75		80
Trp	Trp	Leu	Arg	Ser	Gln	Glu	Lys	Thr	Arg	Ile	Gln	Leu	Ser	Phe	Asp
					85				90					95	
His	Gln	Phe	Gly	Leu	Glu	Glu	Ala	Glu	Asn	Asp	Ile	Cys	Arg	Tyr	Asp
					100				105					110	

Phe Val Glu Val Glu Val Ser Glu Ser Ser Thr Val Val Arg Gly
 115 120 125
 Arg Trp Cys Gly His Lys Glu Ile Pro Pro Arg Ile Thr Ser Arg Thr
 130 135 140
 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
 145 150 155 160
 Pro Gly Phe Lys Ile Tyr Tyr Ser Phe Val Glu Asp Phe Gln Pro Glu
 165 170 175
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Phe Ser Gly
 180 185 190
 Val Ser Tyr His Ser Pro Ser Ile Thr Asp Pro Thr Leu Thr Ala Asp
 195 200 205
 Ala Leu Asp Lys Thr Val Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 210 215 220
 Lys His Phe Asn Pro Val Ser Trp Gln Asp Asp Leu Glu Asn Leu Tyr
 225 230 235 240
 Leu Asp Thr Pro His Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 245 250 255
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Val Lys Arg Tyr Ser Cys
 260 265 270
 Thr Pro Arg Asn His Ser Val Asn Leu Arg Glu Glu Leu Lys Leu Thr
 275 280 285
 Asn Ala Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 290 295 300
 Asn Cys Gly Cys Gly Thr Val Asn Trp Lys Ser Cys Thr Cys Ser Ser
 305 310 315 320
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Lys Phe Glu Pro Gly
 325 330 335
 His Phe Lys Arg Arg Gly Lys Ala Lys Asn Met Ala Leu Val Asp Ile
 340 345 350
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
 355 360 365
 Pro Arg
 370

<210> 5

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC21,987

<400> 5
caacctgttg tttgtcccgtaacc 24

<210> 6
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC21,120

<400> 6
tccagagcataccgcaatcag agtg 24

<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC26317

<400> 7
atcacacctcac agacttgtac cagag 25

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC26318

<400> 8
cctacaaatgc tcattttctgc ttcc 25

<210> 9
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 9
Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln
1 5 10 15
Ile Lys

<210> 10
<211> 25
<212> PRT
<213> Artificial Sequence

<400> 10
Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro Arg
1 5 10 15
Tyr Arg Gly Arg Ser Tyr His Asp Cys
20 25

<210> 11
<211> 24
<212> PRT
<213> Artificial Sequence

<400> 11
Cys Phe Glu Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met
1 5 10 15
Ala Leu Val Asp Ile Gln Leu Asp
20

<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 12

Glu Tyr Met Pro Met Glu

1

5

<210> 13

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 13

Glu Tyr Met Pro Thr Asp

1

5